Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of the Claims:

1. (Currently amended) A method of establishing a map of one or more protein-protein interactions ~~interaction map~~ for comparison of pathophysiological processes or one or more physiological processes comprising

(a) screening for a protein-protein interaction between at least one protein and a plurality of proteins, where the screening is performed in the absence of a simulated redox state perturbation, and where the plurality of proteins are screened concurrently;

(b) screening for a protein-protein interaction between the at least one protein and a plurality of proteins, where the screening is performed in the presence of a simulated redox state perturbation, and where the plurality of proteins are screened concurrently; and

(c) generating the protein-protein interaction map by identifying at least one different protein-protein interaction between (a) and (b), wherein the at least one different protein-protein interaction between (a) and (b) is involved in one or more pathological processes or one or more physiological processes.

2. (Currently amended) The method of Claim 1, wherein the simulated redox state perturbation is generated by a process selected from the group consisting of: variation of concentration of redox state modifier molecules from physiological state, variation of glucose concentration from physiological state, presence of metal ions, ~~alteration in NAD^+/NADH ratio,~~ and oxygen concentrations less than room air.

3. (Previously presented) The method of Claim 1, wherein the simulated redox state perturbation is generated by addition of a redox state modifier molecule selected from the group consisting of superoxide, peroxides, hydrogen peroxide, alkoxides, sulfoxides, brominating species, chlorinating species, nitrosating molecules, nitric oxide, S-nitrosothiols, nitrating molecules, peroxynitrite, NO^- generating molecules, glutathione-regulating enzymes, NADH-regulating enzymes, and flavin-regulating enzymes.

4. (Cancelled)

5. (Currently amended) A method of correlating protein-protein interaction(s) involved in one or more pathophysiological processes or one or more physiological processes with oxygen tension comprising

(a) screening for a protein-protein interaction between at least one protein and a plurality of proteins, where the screening is performed in room air, and where the plurality of proteins are screened concurrently;

(b) screening for a protein-protein interaction between the at least one protein and a plurality of proteins, where the screening is performed in the presence of decreased oxygen tension from that in room air, and where the plurality of proteins are screened concurrently; and

(c) correlating the protein-protein interaction(s) with oxygen tension by identifying at least one different protein-protein interaction between (a) and (b), wherein the at least one different protein-protein interaction between (a) and (b) is involved in one or more pathophysiological processes or one or more physiological processes.

6. (Previously presented) The method of Claim 5 where the at least one protein is associated with a physiological process or a pathophysiological process.

7. (Previously presented) The method of Claim 5 where a plurality of determinations are made in step (b) with different oxygen tensions being employed in each determination.

8. (Currently amended) The method of Claim 5 where the oxygen tensions employed [[are]] in step (b) range from 0.1 mm Hg to 145 mm Hg.

9. (Previously presented) The method of Claim 5 where the different interactions in step (c) are used to identify protein functions associated with a pathophysiological process.

10-17. (Cancelled)

18. (New) A method of establishing a protein-protein interaction map comprising

(a) screening for a protein-protein interaction using a yeast two hybrid system between at least one protein and a plurality of proteins, where the screening is performed in the

absence of a simulated redox state perturbation, and where the plurality of proteins are screened concurrently;

(b) screening for a protein-protein interaction using a yeast two hybrid system between the at least one protein and a plurality of proteins, where the screening is performed in the presence of a simulated redox state perturbation, and where the plurality of proteins are screened concurrently; and

(c) generating the protein-protein interaction map by identifying at least one different protein-protein interaction between (a) and (b).

19. (New) The method of Claim 18, wherein the simulated redox state perturbation is generated by a process selected from the group consisting of: variation of concentration of redox state modifier molecules from physiological state, variation of glucose concentration from physiological state, presence of metal ions, and oxygen concentrations less than room air.

20. (New) The method of Claim 18, wherein the simulated redox state perturbation is generated by addition of a redox state modifier molecule selected from the group consisting of superoxide, peroxides, hydrogen peroxide, alkoxides, sulfoxides, brominating species, chlorinating species, nitrosating molecules, nitric oxide, S-nitrosothiols, nitrating molecules, peroxynitrite, NO^- generating molecules, glutathione-regulating enzymes, NADH-regulating enzymes, and flavin-regulating enzymes.

21. (New) A method of correlating protein-protein interaction(s) with oxygen tension comprising

(a) screening for a protein-protein interaction using a yeast two hybrid system between at least one protein and a plurality of proteins, where the screening is performed in room air, and where the plurality of proteins are screened concurrently;

(b) screening for a protein-protein interaction using a yeast two hybrid system between the at least one protein and a plurality of proteins, where the screening is performed in the presence of decreased oxygen tension from that in room air, and where the plurality of proteins are screened concurrently; and

(c) correlating the protein-protein interaction(s) with oxygen tension by identifying at least one different protein-protein interaction between (a) and (b).

22. (New) The method of Claim 21 where the at least one protein is associated with a physiological process or a pathophysiological process.

23. (New) The method of Claim 21 where a plurality of determinations are made in step (b) with different oxygen tensions being employed in each determination.

24. (New) The method of Claim 21 where the oxygen tensions employed in step (b) range from 0.1 mm Hg to 145 mm Hg.

25. (New) A method of establishing a protein-protein interaction map comprising

(a) screening for a protein-protein interaction between at least one protein and a plurality of proteins, where the screening is performed in the absence of a simulated redox state perturbation, and where the plurality of proteins are screened concurrently;

(b) screening for a protein-protein interaction between the at least one protein and a plurality of proteins, where the screening is performed in the presence of a simulated redox state perturbation, and where the plurality of proteins are screened concurrently;

(c) generating the protein-protein interaction map by identifying at least one different protein-protein interaction between (a) and (b) and

wherein the simulated redox state perturbation is generated by a process selected from the group consisting of: variation of concentration of redox state modifier molecules from physiological state, variation of glucose concentration from physiological state, presence of metal ions and decreased oxygen tension from that in room air wherein a plurality of determinations are made in step (b) with different oxygen tensions being employed in each determination.

26. (New) The method of Claim 25, wherein the simulated redox state perturbation is generated by addition of a redox state modifier molecule selected from the group consisting of superoxide, peroxides, hydrogen peroxide, alkoxides, sulfoxides, brominating species, chlorinating species, nitrosating molecules, nitric oxide, S-nitrosothiols, nitrating molecules, peroxynitrite, NO^- generating molecules, glutathione-regulating enzymes, NADH-regulating enzymes, and flavin-regulating enzymes.

27. (New) A method of correlating protein-protein interaction(s) with oxygen tension comprising

(a) screening for a protein-protein interaction between at least one protein and a plurality of proteins, where the screening is performed in room air, and where the plurality of proteins are screened concurrently;

(b) screening for a protein-protein interaction between the at least one protein and a plurality of proteins, where the screening is performed in the presence of decreased oxygen tension from that in room air, and where the plurality of proteins are screened concurrently;

(c) correlating the protein-protein interaction(s) with oxygen tension by identifying at least one different protein-protein interaction between (a) and (b) and

wherein a plurality of determinations are made in step (b) with different oxygen tensions being employed in each determination.

28. (New) The method of Claim 27 where the at least one protein is associated with a physiological process or a pathophysiological process.

29. (New) The method of Claim 27 where a plurality of determinations are made in step (b) with different oxygen tensions being employed in each determination.

30. (New) The method of Claim 27 where the oxygen tensions employed in step (b) range from 0.1 mm Hg to 145 mm Hg.